

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hermeking, Heiko
Vogelstein, Bert
Kinzler, Kenneth

(ii) TITLE OF THE INVENTION: 14-3-3 SIGMA ARREST THE CELL
CYCLE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Banner & Witcoff
(B) STREET: 1001 G Street, NW
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20001

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 18-DEC-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kagan, Sarah A
(B) REGISTRATION NUMBER: 32141
(C) REFERENCE/DOCKET NUMBER: 1107.72886

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-508-9100
(B) TELEFAX: 202-508-9299
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGAGACACA	GAGTCGGCA	TTGGTCCCAG	GCAGCAGTTA	GCCGCGGCC	CGCCTGTGTG	60
TCCCCAGAGC	CATGGAGAGA	GCCAGTCTGA	TCCAGAAGGC	CAAGCTGGCA	GAGCAGGCCG	120
AAACGCTATGA	GGACATGGCA	GCCTTCATGA	AAGGCGCCGT	GGAGAAGGGC	GAGGAGCTCT	180
CCTGCGAAGA	GCGAACCTG	CTCTCAGTAG	CCTATAAGAA	CCTGGTGGGC	GGCCAGAGGG	240
CTGCCTGGAG	GGTGTGTGTC	AGTATTGAGC	AGAAAAGCAA	CGAGGAGGGC	TGGAGGAGA	300
AGGGGCCGGA	GGTGTGTGAG	TACCGGGAGA	AGGTGGAGAC	TGAGCTCCAG	GGCGTGTGCG	360
ACACCGTGCT	GGGCTGCTG	GACAGCCACC	TCATCAAGGA	GGCCGGGGAC	GCCGAGAGCC	420
GGGTCTTCTA	CCTGAAGATG	AAGGGTACT	ACTACCGCTA	CCTGGCCGAG	GTGGCCACCG	480
GTGACGACAA	GAAGCGCATC	ATTGACTCAG	CCCGGTCAAGC	CTACCAGGAG	GCCATGGACA	540
TCAGCAAGAA	GGAGATGCCG	CCCACCAACC	CCATCCGCCT	GGGCCTGGCC	CTGAACCTTT	600
CCGTCTTCCA	CTACCGAGATC	GCCAACAGCC	CCGAGGAGGC	CATCTCTCTG	GCCAAGACCA	660
CTTTCGACGA	GGCCATGGCT	GATCTGCACA	CCCTCAGCGA	GGACTCCTAC	AAAGACAGCA	720
CCCTCATCAT	GCAGCTGCTG	CGAGACAAACC	TGACACTGTG	GACGGCCGAC	AACGCCGGGG	780
AAGAGGGGGG	CGAGGCTCCC	CAGGAGCCCC	AGAGCTGAGT	TGTGCCCGCC	ACCGCCCCGC	840
CCTGCCCCCT	CCAGTCCCCC	ACCTGCGGA	GAGGACTAGT	ATGGGGTGGG	AGGCCCCACC	900
CTTCTCCCCCT	AGGCCTGTT	CTTGCTCCAA	AGGGCTCCGT	GGAGAGGGAC	TGGCAGAGCT	960
GAGGCCACCT	GGGGCTGGGG	ATCCCACCT	TCTTGCAGCT	TGTGAGCGCA	CCTAACCACT	1020
GGTCATGCC	CCACCCCTGC	TCTCCGCACC	CGCTTCTCC	CGACCCCAAGG	ACCAGGCTAC	1080
TTCTCCCCCTC	CTCTTGCCCTC	CCTCCTGCC	CTGCTGCCTC	TGATCGTAGG	AATTGAGGAG	1140
TGTCCCGCCT	TGTGCTGAG	AACTGGACAG	TGGCAGGGGC	TGGAGATGGG	TGTGTGTGTG	1200
TGTGTGTGTG	TGTGTGTGTG	CGCGCGCGCC	AGTGCAAGAC	CGAGACTGAG	GGAAAGCATG	1260
TCTGCTGGGT	GTGACCATGT	TTCCTCTCAA	TAAGTTCCC	CTGTGACACT	CAAAAAAAA	1320

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Arg	Ala	Ser	Leu	Ile	Gln	Lys	Ala	Lys	Leu	Ala	Glu	Gln	Ala
1				5				10					15		
Glu	Arg	Tyr	Glu	Asp	Met	Ala	Ala	Phe	Met	Lys	Gly	Ala	Val	Glu	Lys
				20				25					30		
Gly	Glu	Glu	Leu	Ser	Cys	Glu	Glu	Arg	Asn	Leu	Leu	Ser	Val	Ala	Tyr
				35				40					45		

Lys Asn Val Val Gly Gly Gln Arg Ala Ala Trp Arg Val Leu Ser Ser
 50 55 60
 Ile Glu Gln Lys Ser Asn Glu Glu Gly Ser Glu Glu Lys Gly Pro Glu
 65 70 75 80
 Val Arg Glu Tyr Arg Glu Lys Val Glu Thr Glu Leu Gln Gly Val Cys
 85 90 95
 Asp Thr Val Leu Gly Leu Leu Asp Ser His Leu Ile Lys Glu Ala Gly
 100 105 110
 Asp Ala Glu Ser Arg Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr Tyr
 115 120 125
 Arg Tyr Leu Ala Glu Val Ala Thr Gly Asp Asp Lys Lys Arg Ile Ile
 130 135 140
 Asp Ser Ala Arg Ser Ala Tyr Gln Glu Ala Met Asp Ile Ser Lys Lys
 145 150 155 160
 Glu Met Pro Pro Thr Asn Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe
 165 170 175
 Ser Val Phe His Tyr Glu Ile Ala Asn Ser Pro Glu Glu Ala Ile Ser
 180 185 190
 Leu Ala Lys Thr Thr Phe Asp Glu Ala Met Ala Asp Leu His Thr Leu
 195 200 205
 Ser Glu Asp Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg
 210 215 220
 Asp Asn Leu Thr Leu Trp Thr Ala Asp Asn Ala Gly Glu Glu Gly
 225 230 235 240
 Glu Ala Pro Gln Glu Pro Gln Ser
 245

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCCAGC	CTGCCCCCTCC	ACTTCTCTCC	CAAGCCAGGT	CCCGGCATGG	GTGGGTTATG	60
CTCATGCTGG	CAATACTTGA	AACGGGTTA	TTAATGCTGG	GTATTTGCA	CAATTTATA	120
GACCTCTTT	CTACATAGTC	TTTTTAAAT	GGAAGGAGAA	AATGTCAGCC	ACATTACTGT	180
CTGTGTAGTG	CCAGGTGAAG	GGTTATCAGA	AGGCTGGTTG	GTTTAATAA	GTTTATTCCA	240
AGAGACCTTC	TGGCTGGAAT	GAGTGGAGGT	GTGTGTGCAT	GTGTGTGTGT	GTTCATGTGT	300
GCCCTGTATG	AATGTGGCTG	GCTCCCAGAT	CCCCTGGGCT	GCCCCCTGCC	CCATCCCCTT	360
TGAGTATCAG	AAGCACTCTG	AGCCAAGGGG	ACAGGGGGCA	CGTGCACGTG	TCACGAGAAA	420
ACCCCTGGGCT	CCCACGGGG	CTCAGCCCAG	CCTCCTATCT	TTCCCTCTTC	TATGGACTTC	480
AGACAGCCAG	TGTCTGGGGA	CTCTGCCACT	CTACCCCCAG	CCCTACCCAC	CAGCCCCCAG	540
GTGAGGCTTC	CAGCTGGGAC	CTGCCAGAC	AGGCTGAGCC	TGGGCGTGGT	GGGTGGGTG	600
ATGGCTCTGG	GGAGCGGCTG	CCATCCTACA	AGCCACACCC	CCTCCTCTGA	GCTCTGAATA	660
TGGGACCCAG	TGCCAGGAGC	TGGAAGACAA	GGTGTCTCTG	CCAAACGGGA	CCTCCATCCA	720
GAGAAAAGGA	AGAAGGTGCA	GGGTGGGCCA	AGAGGCAAGT	GAAGGTTGGC	CTGAGTCTGG	780
GCCGGAAACT	CAGAGGATGT	TTCTCCTCTG	CTGGGAGCTG	TAGTTTCTTA	TCAAAATAGA	840

TATTGTTCCA	CCATCCCCCT	CCCTGGCCCT	TCAAGTGGGC	TGAAGCCTTG	GAAAGTGACA	900
TAGGAAGTCC	CCAGATCTTG	CCCTTCTCAC	TCCAGAGGCT	AGTGGTCACA	GACAGCTGGG	960
AATGGCAGCC	ACAGAGGGTC	CCTCTGGAGA	AACAGCTCA	CCCCAGCCTC	AGGGCCCTGG	1020
GCATCACTGC	AGTGGCCCTG	GGAGGTGAGG	AAGAAGCTGG	CTAGAGGAGG	GGGCTCCAC	1080
CTACCTTTA	TTAAGCCAG	TATTCTTGT	TCCTGCTTGT	AATAAAACTT	CAGTTTATAA	1140
GAGTTGCTT	GCTTGGTTT	GGTTTTGTT	TGCTTTTCCCT	TTGCTGAGGC	CCCAACTGGG	1200
AGCCCTCTGT	TCTTCAGAC	AAATTTGGTT	CTTCCTGGG	GAGACTGTGA	GAAGGCAGGC	1260
AGCCCAGTGA	TCTGGCTACA	TTTCCCTCA	CCTGGCTGGA	GCTCTGTCCG	CTGGAGGAAG	1320
AGCAGAGAGG	GCTGCGGCTG	AGCCCCCATG	GGCACGTGAA	AAGAGGCCAT	CCTGTCCCCCT	1380
CTTGTCCCC	TCCACCTTCC	CTGCCTCAG	GGGCTTGGAG	ACCCCAAATT	CTTCTTCCCT	1440
ACTGCCTTTC	CACTCCGATC	CCCAATGAGT	CCCCAGCTAA	AAAATGTTT	GAGACAGTAG	1500
ATTCCAGTTT	GAGAGCCGA	GCTTCCCTGG	CTACACACTC	CAACCTGGC	ACCAGGGCCC	1560
AGCCAGACAA	CTCATAACAC	TGGCCCACCT	CTCTGGTATC	TCCCTCAGGA	GGACACCTGT	1620
CAGGATTTG	CCATCTCTG	CACAGCCTGA	GGGGAGCTAA	CAGGCCTCTT	TGCAAGAGGGT	1680
TAGCTGGTAA	GACC GTTTCT	TCCTGTCTGG	CCAGCACTGC	CCGCTCCCCCT	CCACACACCA	1740
TCTCATCTC	ATCCGATGCC	TCGCAAACCC	CATGGAGGCC	GTCCATCTGT	CTGGTGTGTG	1800
GTGCGGTGTG	TGTGCTGGTG	GTGGTAGGCT	CTCCAGGGAC	TCCCCGCTAA	GCAGAAGGAT	1860
CGGGATATAG	GGCAAGGCTA	AAAGCCCAGC	CCCATTGTGG	ACTGAGGAAG	TACGTTCGCG	1920
CAGAGCAGCT	CTCCAGCTGG	AAGAGGAGGT	GGAGGGTGTAG	GCTGGGGAGA	GGATGGCGAA	1980
CCTGCCCTGA	GGTGCTTGGG	TCTGTCTGG	TGGGGTCTG	GTATGCAGGG	GCCACCCGTC	2040
ACTAACACTC	TTATGTCCTG	GCTTCTGTG	CCCGCTGAGC	TTTCTCTCAC	CCGCCCCGTTT	2100
TCTCTCTGC	TTCATGGCT	GTCGCCCTAAG	CCTTGGCCCT	TCTCTGGG	AGAGGCAGGT	2160
GCTGTGGCAG	CACCTCTCCC	CACCAACGGG	CCCCCTGCAGG	CCGCCTCCCT	CCTCCCAGGC	2220
CTGCTAACCC	TCTCTCTTCT	CCTCTTTGC	TGICCTGCG	GGGATCTCCA	GTGTGTGCGG	2280
GGGCTTAAGG	ACCTCCCTGAG	GACCGCTGCT	CTCTGCCCTCT	CCAGGAATGG	CCTGGGGGGA	2340
GCCAGGCACC	CGGCACCTCTC	ACCTGCCCTAA	CCTGTGGCCC	ATCTGCCACC	ATCTGTGCCT	2400
ACAGGGTCTG	CCCCCCCAGCC	TGCCCCGCC	GTGTGCTCTC	TAGGACCCCCA	TAGGGGGCAG	2460
GGGCTGGCCT	CTTGCCCCA	TTCCCCTGCTC	ATGCCGGCCA	GAGTGTAGAA	AGCCATAACG	2520
CACGCAGCCA	TCAGCACAAT	AATGTGACTC	TACGCTGATA	TGCTCCCTCT	CTCCTCCACT	2580
GACTTCCCCCT	TCCCCGGATT	GTGAGGTGTC	AAGACTAGGA	ATCTGGCCTT	AGAGCCTGCC	2640
CCTCCACCCCC	CTCAGATCAG	GCATAGCCAT	AGTCAAGCCC	AGCAGGTTTC	CTCAGGAGCT	2700
GTCTGGGTG	TTGATGGTGG	ATGACGCTG	TGAACAAGTT	TGGTGACTGT	TCTAACGACA	2760
ACTGGCTTGA	TACTGTTCCC	ACGGCCTGTC	CACCTCCCAC	CCCCAACCC	CCACCAAGAGT	2820
AGGTAGGATG	TAGGGAGGGT	CGGTGCCGCC	TTGCTCTAG	GCACTGAGGG	ACCAAGCTAG	2880
CCGTGCACAG	CCCCATACAC	TTCAGGGCG	TAAAGGAAAG	AGCTGAGCCA	AGGAAAATCA	2940
GCTGAGCCCA	GGGCTGGGGG	CTGCTTGCT	GCTATCTGT	ACCTTTTTT	TTTTAACCA	3000
AAATAAAAGAT	TCCCCCTTTC	TTGCCATACC	ATTGGCTGTC	TGGTGGCGCC	TTTACTTTGG	3060
GGCCCAGGGA	TGGGACCTGC	AGTGGCGTG	TGGAACATAT	GGCTCCCCCT	CGCTCCCAGC	3120
TTTCTTCCAG	CTGGCCAGTG	CTGCTCTGG	GATTACAAG	CACAACGAAG	CCAGGAGGG	3180
CACAGGAAA	GTGGCTGACA	TCCTTTCAC	TCTGCCCTC	CAGAACTCTT	GGTCTCAATT	3240
CCAGACACCA	CCCAGCCTTA	GCTGACCTCT	GGATTCTGAT	AGGTCCCAGT	GCAGGCTGAG	3300
ACAGAGGGTT	TAACCTCCAGT	TTGGGACTGC	CATACCCATG	AACTGAGCCC	AGCCCAGGGT	3360
AACGATCTCA	TGGAAACTTC	TCTCTCCCCA	GTTGCTGCAC	TACATCAAGA	TACACACATG	3420
TGCATACACT	GTACTATGGG	CTAAAAAAAT	ACGTACCGCT	ACCGTTCA	AAGGGCTTGC	3480
CGAGTCCCGG	GCCCCATTTC	TCATCTTAAC	CTGTGAGGAG	GATGATGTCA	GCCTTTTTAC	3540
AGATGAGGGA	ACTGAGACTC	AAGGAAGAAA	CAGGAGCTGC	CCAAGTCAC	CCAGCTGGCA	3600
AAGCAGCAAA	TCCCAGATCG	GAACCTGATC	TCTGCCCTGA	GCTCTGAGCC	ATCTGCACTA	3660
CCCAAGGAAT	GAATACAGCG	GTGGGAGGAT	GAGATCTTGG	AGAAACCC	CTAAATTAGAGA	3720
ATGTCATAGC	CAGTAGAGGG	CTTAGAGTTG	ATCTGGGCCA	GCCTCCTGT	TTTACTGATG	3780
GAGAAATTGA	AGCCCAGAGG	CAGGAAGGGA	CCTGCCCAAG	GCCTTATAAC	AGAGCTGGGA	3840
TGCAGTCCCA	CACTCTGACC	TCATTCCATT	CTCTCTCCAT	AAATTCTGCA	CTGTCCTAG	3900
ACTGGACTGG	TTTAGATGTG	GGATACTCTA	AACAGCAGTG	CCTTCAAGAG	AAAAAGAATC	3960

AGAAACTACGA	ATCACTTAAA	AGTAATGTAA	GCTACTCTGG	GCACACTGCC	TATGGGGTCC	4020
CCCTGCTCCA	CAAGGAGCCA	CAAAAATAAT	TAAAATAATT	TAATATCCCT	TCCCAAAGGT	4080
AACCAGTAAA	GTAAGCTCTT	GGCTAGGTAA	CTGGACTCTT	GTTCACAACT	AGCCAGTGGG	4140
AAAAGGTGCT	AGAGCTTCTT	CTGGCCACCT	GTAAATTG	ATCATTCCAA	GACAGAAACA	4200
TTTCTTAGGA	AGTTCTTCTT	AGAATCTACC	TGGTGTCCCT	CCCACGTGCTA	TCAGAGCCCT	4260
GTCCCTCTGTC	CTCAGTGGAG	GTAGAGAGCA	AATGGTTGCT	GCTTTCTTCA	TCACAAACCT	4320
TCAAAGCCTA	TTATTACCAAG	CTAAGAAGGA	TTGGTTGACT	ATGGGCCAGA	GCCCCTGAGC	4380
CTGCTGGTAG	AATGGATGCT	GTACAGGAGG	GTGGGGAGGT	AGCAGGCAGA	ATGAGGAAAG	4440
CCCCTTTGAG	CTGCAACCCC	AGCTCCTGTC	CTGCTGACTC	AGACAGCTGA	CTGTGGAGCT	4500
CCATGCCCTG	CCAGGGCCTG	CTGCCTCCTG	CCCGTCTGAG	CTCCTGAACT	TGGGAAATGG	4560
AGGCCCAGAG	GCAAAGGGAG	GTACCTGAGA	CAGGAACCTGA	GTCAGGATCA	ACAGGCCAGA	4620
GCGGGCAGGA	GGTATCAGGC	AGCCTGGCTC	CCAGATGCAC	CCCTGAGCTC	CAGCAGGGGA	4680
GGAGTAGGAA	TGAAGGGGCT	TCCTTGCCTC	TGCTCATGGC	TATGCGGAGG	CGGTGAACCA	4740
CCACCAGGTC	CTCTGGCTTA	AGTGGCGGGGA	AGCAAATGGT	CCCTCCCTGG	ACTCAGGCTC	4800
CAAAGTTCTT	GGGCCTGCCT	TCCAGGTTCC	CAGTGTCTG	GGATCTCCAG	CTTTCCCCAG	4860
GACTTGGGGA	AGCCCCGGCT	GGATGACTAG	TACAAATGAA	GGCCCTTGAG	GTTCCAGGAC	4920
CTGCTGAGGT	CACAGGAATA	TCCTAGATCA	AGCTTGCTCA	ACCCACGGCC	CACAGGCTGC	4980
ATGTGGCCCA	GAATGGCTT	GAATGCAGCC	CAACACAAAT	TAGTAAACTT	TCTTAAACAA	5040
TTATGAGATT	TTTTTGCAAA	TTTTTTTTTT	TTTTTTAGCT	CATCAGTTAT	TGGTAGTGT	5100
GGTATATTCTT	ATGTGTGGCC	CAAGACAATT	CTTCCAATGT	GGCCCTAGGG	AGCCAAAAGA	5160
TTGGACACGC	CTGTCCCTAGA	TGGAGAGGAA	GGAGGCAGTG	CTGAGCACAT	CTGGCCATT	5220
ATCCATCTGG	AGAGAGAAGG	CTATGGGCAA	ACTGCTTCC	CTCCCCGTGA	GACACCCAGC	5280
TGGGAAGGTC	TGGCCTTGG	TAAGTCTCTG	CTTGGGGTCC	TTCCCTCATT	CACAGAACCT	5340
AACTCTATGT	TAGTGCTTTG	TGAGTATATG	TTGATCATAA	TAAAGTTGAC	GGGATT	5400
CACATGATAA	TAATAGTTGT	CATCTGGCCG	GGCATGGTGG	CTTATGCCTA	TAATTCAGC	5460
ACTTTGGAAG	GCTGAGGCAG	GTGGATCACT	TGAGGTCAGC	TGTTGAGAC	CAGCCTGGCC	5520
AAACATGGTGA	AACCACATCT	CTACTTAAAA	AAAAAAA	TACAAAAATT	AGCTGGGTGT	5580
GGTGGTGCAC	CCTTGTAAATC	CCAGCTACTC	GGGAGGCTGA	GGCAGGAGAA	TCACTTGAAC	5640
CCAGGAGGTG	GAGGTTGCAG	TGAGCTGAGA	TTGTGCCACT	ACACTCCAGC	CTGGGTGACA	5700
AGAGC GAAAC	TCCGTCTCAA	AAAAAAAGAA	AATAATAATA	ATAATAGTTG	CCATCCATT	5760
TACTGTGCTT	TCCATTAACT	CGTGTAAATCC	TCACAAGTCC	CATTTTATAG	TTACAGGAAC	5820
TGAGGCTCAC	AGAGCTTAAA	TCACTTGGCC	AAGGCCACAA	ACAGCTATAA	GAATTACATT	5880
TAGGCAGTCT	GATTCCAAAG	ATACTAGTCT	ATTCTGTATC	TCATAGACAA	ACAATACATA	5940
TTCAC TTTT	TGTTGTTGTT	TTGTTTGAG	ACGGAGCTT	GCTCTGTAC	CCAGGCTGGA	6000
GTCCGAGTGGC	GCCATCTCGG	CTCACTGCAA	CGTCCGCC	CCGGGTTCAA	GCGATTCTCC	6060
TGCCCTAGCC	TCCCGACTAG	CTGGGACTAC	AGGCATGTGC	CACCATGCC	GGCTAATT	6120
TTGTATTTT	AGTAGAGACA	GGGTTTCC	GGGTTAGCCA	GAATGGTCT	GATCTCCTGA	6180
CCTTGTGATC	CACCCACCTC	AGCCTCCCAA	AGTGCTGAGA	TGACAGGCGT	GAGCCACCGC	6240
GTCCGACCTA	TATTCACTAT	TTATAAATTG	GAGAGAATAA	GAAAATCAA	AGGGCCAGGT	6300
GTAGTGACTC	ACACCTGTAA	TCCCAGCACT	TTGGGAAGCC	AAGGCAGGAG	GATTGCTTGA	6360
ACCCAGAAGT	TCGAGACCAAG	CCTGGGCAAC	ATGGTGAGAC	CCTGTCTCTA	AAAAAAATAC	6420
AAAAAATTAGC	TGGGCGTTGT	GGTGAGCACC	TTATTCTTAG	GAAGCTGAGG	CAGGAGGATC	6480
ACCTGAGGCC	AAGGAGGTTG	AGACTGCAGT	GAGCTGTGAT	CATACCACTG	TACTTCAGCC	6540
TGGACATCAG	AGTAAGACCC	TATCTCTAAA	AAGGAAATTG	AGAAGAAAGA	AAATCAAAGG	6600
GAAGCAAAT	CACTCACTCT	CACTACCTCA	AGATACCTC	TAGAAGTTGG	TATTTAGTG	6660
TGGTTCTAT	TGTTTCTGT	GTCACTCTC	TGATTTGAGC	AAAATCTTG	GGACGTCAA	6720
CTTAAAATCC	CCTTTACTTC	CTTGGAAACC	CTGTAGCATT	AGCCCAAGACA	TGTCCCTACT	6780
CCTCCCTGTG	GCAAAGAGAA	GGATCTCGTC	TTTGGTCCCC	AGAGTCTGG	CCTAACGCCTC	6840
CCTCCAGGAG	GGAAAGATGAG	TGTTCAGACA	CTCAGAGTAG	CTGGGGGAGA	CACAGGCCTG	6900
TGAAATTATC	CTGGCTAAC	TATTAGGTG	GCAGAACCCC	AGTGAAGGG	GCCCTACCTC	6960
TGAGCCCCAT	CTAACGCTT	GCTATGGGTG	GGGCAGATAA	GCAGGAATCC	ATCCCTATAG	7020
GCTCAATGCC	AACACCCCTA	GGTGAAACTC	TTGATGAAAC	TTGAGGCCAG	GGCTCCGGCA	7080

AGCAGGGAAA	GAACGTTGGC	AACAGAGGTC	TCCATCTCTG	AGGACTCTGC	CAGGGGTCAG	7140
AGATGGGCA	ATGGTCAAAA	GGAGGAACA	GGCCAGGCAC	AGTGGCTCAT	GCCCATAATC	7200
CCAGCACTT	GGGAGGCTGA	GGCAGGAGGA	TCGCTTGAGC	CCAGGAGTTT	GAGACCTGCC	7260
TGGGCAATGT	AGTGAGATCT	GCTCTCTATT	TAAAAAAA	AAAAGGAAA	GAACAAGTAA	7320
ACTTCTGAGA	AACAGGCTGG	GGGAGGCATC	ACGTAGCTGG	AATTGCTGCC	CCATAAAACA	7380
GAATGGTATG	TGTCACTGCC	ACCTCCCTT	CTCAGTCCTC	TCTCTCCCCA	GGTTGCTAGC	7440
GTCCCCCTGG	GGGATCAAAC	TGGACTGCTT	CCCAGCCTCA	GACAGAGAGC	AGTCTGAGTC	7500
AGGCAGGGAAA	GTGGGACAGC	CGGGGAGCTG	GACCCCACCC	TCTGTGAGCC	CCGCTGGTAC	7560
CTGATGGCAT	GTGGCTTGGA	GAGGGCAGGT	GACCTGGCGT	GGAGGGCCAG	AGGGTAAATC	7620
CTCAAACAAG	TGGCAACAGG	CCACCAAAC	T GAAAGGGAAA	ATTGTGTAGT	GATGGGAAAT	7680

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGCATGTGC CACCATGCC

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTAGCATTAG CCCAGACATG TCC

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